

SEQUENCE LISTING

<110> Falco, Saverio Carl
Hitz, William D.
Kinney, Anthony J.
Cahoon, Rebecca E.
Rafalski, J. Antoni

<120> PLANT BRANCHED CHAIN AMINO ACID BIOSYNTHETIC ENZYMES

<130> BB-1126

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<150> 60/063,423

<151> 1997 October 28

<160> 54

<170> Microsoft Word Version 7.0A

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<211> 2135

<212> DNA

<213> Zea mays

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 <213> Zea mays

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 Gln Gly Ala Ser Gln Ala Val Leu Tyr Gly Val Gly Leu Thr Asp Ala
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 Asp Leu Arg Lys Pro Gln Val Gly Val Ser Ser Val Trp Tyr Glu Gly
 65 70 75 80
 Asn Thr Cys Asn Met His Leu Leu Arg Leu Ala Glu Ala Val Arg Asp
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 Gly Val Arg Glu Ala Gly Met Val Gly Phe Arg Phe Asn Thr Val Gly
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 Val Ser Asp Ala Ile Ser Met Gly Thr Arg Gly Met Cys Tyr Ser Leu
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 Gln Ser Arg Asp Leu Ile Ala Asp Ser Ile Glu Thr Val Met Gly Ala
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 Asp Ile Val Ser Ala Phe Gln Cys Tyr Gly Glu Tyr Val Ser Gly Ser
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 Ile Thr Asp Glu Gln Arg Lys Asn Val Leu Arg Asn Ser Cys Pro Gly
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 Ala Gly Ala Cys Gly Gly Met Tyr Thr Ala Asn Thr Met Ala Ser Ala
 225 230 235 240
 Ile Glu Thr Leu Gly Met Ser Leu Pro Tyr Ser Ser Ser Thr Pro Ala
 245 250 255
 Glu Asp Pro Leu Lys Leu Glu Glu Cys Arg Leu Ala Gly Lys Tyr Leu
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 Leu Glu Leu Leu Lys Met Asp Leu Lys Pro Lys Asp Ile Ile Thr Glu
 275 280 285
 Lys Ser Leu Arg Asn Ala Met Val Ile Val Met Ala Leu Gly Gly Ser
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 Thr Asn Ala Val Leu His Leu Ile Ala Ile Ala Arg Ser Val Gly Leu
 305 310 315 320

10027450.122001

10027450 133001

His	Leu	Thr	Leu	Asp	Asp	Phe	Gln	Lys	Val	Ser	Asp	Gln	Pro	Phe		
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Lys	Ile	Gly	Gly	Thr	Pro	Ala	Val	Ile	His	Tyr	Leu	Leu	Glu	Gln	Gly	
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Asn	Ala	Lys	Ile	Phe	Pro	Pro	Leu	Ser	Glu	Gly	Gln	Gln	Ile	Ile	Arg	
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Pro	Leu	Asp	Asn	Pro	Ile	Lys	Pro	Thr	Gly	His	Ile	Gln	Ile	Leu	Tyr	
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Gly	Asn	Leu	Ala	Pro	Glu	Gly	Ser	Val	Ala	Lys	Ile	Thr	Gly	Lys	Glu	
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Gly	Leu	Phe	Phe	Ser	Gly	Pro	Ala	Leu	Val	Phe	Glu	Gly	Glu	Glu	Ser	
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Met	Ile	Thr	Ala	Ile	Ser	Glu	Asn	Pro	Ala	Asn	Phe	Lys	Gly	Lys	Val	
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Val	Val	Ile	Arg	Gly	Glu	Gly	Pro	Lys	Gly	Gly	Pro	Gly	Met	Pro	Glu	
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Met	Leu	Thr	Pro	Thr	Ser	Ala	Ile	Met	Gly	Ala	Gly	Leu	Gly	Lys	Glu	
			485						490					495		
Cys	Ala	Leu	Leu	Thr	Asp	Gly	Arg	Phe	Ser	Gly	Gly	Ser	His	Gly	Phe	
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Val	Val	Gly	His	Ile	Cys	Pro	Glu	Ala	Gln	Glu	Gly	Gly	Pro	Ile	Gly	
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Leu	Val	His	Ser	Gly	Asp	Val	Ile	Thr	Ile	Asp	Val	Ser	Lys	Arg	Val	
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Ile	Asp	Val	Asp	Leu	Thr	Glu	Gln	Gln	Leu	Glu	Glu	Arg	Arg	Arg	Lys	
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 <212> DNA
 <213> Glycine max

<400> 3

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Ala	Ser	Ile	Ala	Val	Glu	Thr	Pro	Thr	Glu	Thr	Val	Lys	Leu	Asn	Lys
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Tyr	Ser	Ser	Arg	Ile	Thr	Glu	Pro	Lys	Ser	Gln	Gly	Ala	Ser	Gln	Ala
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Val	Leu	Tyr	Gly	Val	Gly	Leu	Ser	Glu	Asp	Asp	Met	Ala	Lys	Pro	Gln
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Val	Gly	Val	Ser	Ser	Val	Trp	Tyr	Glu	Gly	Asn	Thr	Cys	Asn	Met	His
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Leu	Leu	His	Leu	Ser	Glu	Ala	Val	Arg	Asp	Gly	Val	Ala	Ala	Ala	Gly
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Met	Val	Pro	Phe	Arg	Phe	Asn	Thr	Val	Gly	Val	Ser	Asp	Ala	Ile	Ser
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Ala	Asp	Ser	Ile	Glu	Thr	Val	Met	Ala	Ala	Gln	Trp	Tyr	Asp	Gly	Asn
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Asp	Glu	Cys	Arg	Leu	Ala	Gly	Lys	Tyr	Leu	Leu	Glu	Leu	Leu	Lys	Met	
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Phe	Gln	Lys	Val	Ser	Asp	Glu	Val	Pro	Phe	Ile	Ala	Asp	Leu	Lys	Pro	
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Met	Thr	Val	Thr	Gly	Lys	Thr	Leu	Ala	Glu	Asn	Ala	Glu	Leu	Val	Pro	
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Lys	Lys	Thr	Ala	His	Ile	Gln	Ile	Leu	Tyr	Gly	Asn	Leu	Ala	Pro	Gln	
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Pro	Ala	Leu	Val	Phe	Glu	Gly	Glu	Glu	Ala	Met	Ile	Ala	Ala	Ile	Ser	
Glu	Asp	Pro	Ser	Ser	Phe	Lys	Gly	Lys	Val	Val	Val	Ile	Arg	Gly	Glu	
Gly	Pro	Lys	Gly	Gly	Pro	Gly	Met	Pro	Glu	Met	Leu	Thr	Pro	Thr	Ser	
Ala	Ile	Met	Gly	Ala	Gly	Leu	Gly	Lys	Glu	Val	Ala	Leu	Leu	Thr	Asp	
Gly	Arg	Phe	Ser	Gly	Gly	Ser	His	Gly	Phe	Val	Val	Gly	His	Ile	Cys	

Pro Glu Ala Gln Gly Gly Pro Ile Gly Leu Ile Gln Asn Gly Asp
530 535 540

Val Ile Asn Val Asp Ile Lys Asn Arg Arg Ile Asp Val Leu Val Ser
545 550 555 560

Asp Glu Glu Met Glu Ala Arg Arg Lys Lys Trp Thr Ala Pro Pro Tyr
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Lys Ala Asn Arg Gly Ala Leu Tyr Lys Tyr Ile Lys Asn Val Thr Pro
580 585 590

Ala Ser Ser Gly Cys Val Thr Asp Glu
595 600

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Ala Ile Ser Glu Asn Pro Ala Asn Phe Lys Gly Lys Val Val Val Ile
35 40 45
Arg Gly Glu Gly Pro Lys Gly Gly Pro Gly Met Pro Glu Met Leu Thr
50 55 60
Pro Thr Ser Ala Ile Met Gly Ala Gly Leu Gly Lys Glu Cys Ala Leu
65 70 75 80
Leu Thr Asp Gly Arg Phe Ser Gly Gly Ser His Gly Phe Val Val Gly
85 90 95
His Val Cys Pro Glu Ala Gln Glu Gly Gly Pro Ile Gly Leu Val Glu
100 105 110

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Asn Gly Asp Thr Ile Thr Ile Asp Val Gly Lys Lys Val Ile Asp Val
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Asp Leu Thr Glu Asp Gln Leu Glu Gln Arg Arg Arg Lys Trp Ser Pro
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Pro Pro His Lys Xaa Thr Asn Gly Ser Thr Leu Glu
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<213> Saccharomyces cerevisiae

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35 40 45

Lys Lys Glu Asp Phe Lys Lys Pro Gln Val Gly Val Gly Ser Cys Trp
50 55 60

Trp Ser Gly Asn Pro Cys Asn Met His Leu Leu Asp Leu Asn Asn Arg
65 70 75 80

Cys Ser Gln Ser Ile Glu Lys Ala Gly Leu Lys Ala Met Gln Phe Asn
85 90 95

Thr Ile Gly Val Ser Asp Gly Ile Ser Met Gly Thr Lys Gly Met Arg
100 105 110

Tyr Ser Leu Gln Ser Arg Glu Ile Ile Ala Asp Ser Phe Glu Thr Ile
115 120 125

Met Met Ala Gln His Tyr Asp Ala Asn Ile Ala Ile Pro Ser Cys Asp
130 135 140

Lys Asn Met Pro Gly Val Met Met Ala Met Gly Arg His Asn Arg Pro
145 150 155 160

Ser Ile Met Val Tyr Gly Gly Thr Ile Leu Pro Gly His Pro Thr Cys
165 170 175

Gly Ser Ser Lys Ile Ser Lys Asn Ile Asp Ile Val Ser Ala Phe Gln
180 185 190

Ser Tyr Gly Glu Tyr Ile Ser Lys Gln Phe Thr Glu Glu Glu Arg Glu
195 200 205

Asp Val Val Glu His Ala Cys Pro Gly Pro Gly Ser Cys Gly Gly Met
210 215 220

Tyr Thr Ala Asn Thr Met Ala Ser Ala Ala Glu Val Leu Gly Leu Thr
225 230 235 240

Ile Pro Asn Ser Ser Ser Phe Pro Ala Val Ser Lys Glu Lys Leu Ala
245 250 255

Glu Cys Asp Asn Ile Gly Glu Tyr Ile Lys Lys Thr Met Glu Leu Gly
260 265 270

10027450 122001

Ile	Leu	Pro	Arg	Asp	Ile	Leu	Thr	Lys	Glu	Ala	Phe	Glu	Asn	Ala	Ile	
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Val	Ala	Val	Ala	His	Ser	Ala	Gly	Val	Lys	Leu	Ser	Pro	Asp	Asp	Phe	
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Gln	Arg	Ile	Ser	Asp	Thr	Thr	Pro	Leu	Ile	Gly	Asp	Phe	Lys	Pro	Ser	
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Gly	Lys	Tyr	Val	Met	Ala	Asp	Leu	Ile	Asn	Val	Gly	Gly	Thr	Gln	Ser	
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Val	Ile	Lys	Tyr	Leu	Tyr	Glu	Asn	Asn	Met	Leu	His	Gly	Asn	Thr	Met	
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Thr	Val	Thr	Gly	Asp	Thr	Leu	Ala	Glu	Arg	Ala	Lys	Lys	Ala	Pro	Ser	
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Pro	Glu	Ala	Ala	Glu	Gly	Gly	Pro	Ile	Gly	Leu	Val	Arg	Asp	Gly	Asp	
		515					520						525			
Glu	Ile	Ile	Ile	Asp	Ala	Asp	Asn	Asn	Lys	Ile	Asp	Leu	Leu	Val	Ser	
	530					535					540					
Asp	Lys	Glu	Met	Ala	Gln	Arg	Lys	Gln	Ser	Trp	Val	Ala	Pro	Pro	Pro	
	545				550					555					560	
Arg	Tyr	Thr	Arg	Gly	Thr	Leu	Ser	Lys	Tyr	Ala	Lys	Leu	Val	Ser	Asn	
				565					570					575		
Ala	Ser	Asn	Gly	Cys	Val	Leu	Asp	Ala								
			580					585								

<210> 8
 <211> 502
 <212> DNA
 <213> Zea mays

<400> 8
cgctgagcaa cccccggcct acacggcgta gctttgcagg aaatggaata cggcgccgctc 60
ctcgccgccc cgccgctcgt cgcacggccg aactggctcc tcctctcgcc gccggccactg 120
gcgcccgtcta ttcagattca gaatcgctct tattcgatct cgtcattccc actaaaggct 180
ggacctgttaa gggcatgcag agcttttagca agcaactaca cgcaaacatc tgaacacagtt 240
gatttgact gggagaacct gggttttggg attgtgcaaa ctgattatat gtatattgct 300
aagtgcggga cagacgggaa tttttctgag ggtgaaatgg tgccttttgg acctatagcg 360
ctgagtccat cttctggagt cctaaattat ggacagggat tgtttgaggg cctaaaggcg 420
tataagaaaa ctgatggatc catcctatta tttcgcccag aggaaaatgc tgagaggatg 480
cggacagggtg ctgagaggat gt 502

<210> 9
<211> 153
<212> PRT
<213> Zea mays

<400> 9
Met Glu Tyr Gly Ala Val Leu Ala Ala Ala Pro Leu Val Ala Arg Pro
1 5 10 15
Asn Trp Leu Leu Leu Ser Pro Pro Pro Leu Ala Pro Ser Ile Gln Ile
20 25 30
Gln Asn Arg Leu Tyr Ser Ile Ser Ser Phe Pro Leu Lys Ala Gly Pro
35 40 45
Val Arg Ala Cys Arg Ala Leu Ala Ser Asn Tyr Thr Gln Thr Ser Glu
50 55 60
Thr Val Asp Leu Asp Trp Glu Asn Leu Gly Phe Gly Ile Val Gln Thr
65 70 75 80
Asp Tyr Met Tyr Ile Ala Lys Cys Gly Thr Asp Gly Asn Phe Ser Glu
85 90 95
Gly Glu Met Val Pro Phe Gly Pro Ile Ala Leu Ser Pro Ser Ser Gly
100 105 110
Val Leu Asn Tyr Gly Gln Gly Leu Phe Glu Gly Leu Lys Ala Tyr Lys
115 120 125
Lys Thr Asp Gly Ser Ile Leu Leu Phe Arg Pro Glu Glu Asn Ala Glu
130 135 140
Arg Met Arg Thr Gly Ala Glu Arg Met
145 150

<210> 10
<211> 794
<212> DNA
<213> Zea mays

<400> 10
tcgagttttt tttttttttt ttttgtatcc cctgtttgga attatttcaa ggaaggttta 60
tctcctatta atttgatcgt tgaggataaa tttcacctgt ccagccctgg tggaactgga 120
ggtgtgaaaa ccattggaaa ctatgcctcg gtactgaaag cacaaaagat tgcaaagggg 180
aaagatatt ctgatgtcct ttatttggat gctgttcattg acaaatatct tgaagaagtc 240
tcttcctgca atatttttgt tgtgaaagac aatgttattt ctacgcctgc cattaagga 300
acaatacttc ctggtataac gaggaaggt atcattgaag ttgctcagag caaaggtttc 360
aaggttgagg agcgtctggt gtgtgtagat gagttgatta acgctgatga agttttctgc 420
acggggactg ctggttggt gtcacctgtg gggagtgtta catatatggg gaaaagggtg 480
gaatatggca accaaggagt cgggtgtcgtg tctcagcaac tatacaagtc acttacaagc 540
ctccagatgg gcaatgtgga ggactggatg ggttggaacca tgcaacttaa tcagtagcgg 600
atcacagata ttgccttggc agatcccga ttattacagc tactgggtgc gatagtttt 660
tttttggcag atccatcttg agcatatttg actgtaccgg tttcccttga gactaagacg 720

aaagtgatct tactgatctt ttgtttcaaa tctaaaacga taaaataaaa tgtgggttgc 780
 aaaaaaaaaa aaaa 794

<210> 11
 <211> 198
 <212> PRT
 <213> Zea mays

<400> 11
 Ser Ser Phe Phe Phe Phe Phe Phe Val Ser Pro Val Gly Asn Tyr Phe
 1 5 10 15
 Lys Glu Gly Leu Ser Pro Ile Asn Leu Ile Val Glu Asp Lys Phe His
 20 25 30
 Arg Ala Ser Pro Gly Gly Thr Gly Gly Val Lys Thr Ile Gly Asn Tyr
 35 40 45
 Ala Ser Val Leu Lys Ala Gln Lys Ile Ala Lys Gly Lys Gly Tyr Ser
 50 55 60
 Asp Val Leu Tyr Leu Asp Ala Val His Asp Lys Tyr Leu Glu Glu Val
 65 70 75 80
 Ser Ser Cys Asn Ile Phe Val Val Lys Asp Asn Val Ile Ser Thr Pro
 85 90 95
 Ala Ile Lys Gly Thr Ile Leu Pro Gly Ile Thr Arg Lys Ser Ile Ile
 100 105 110
 Glu Val Ala Gln Ser Lys Gly Phe Lys Val Glu Glu Arg Leu Val Cys
 115 120 125
 Val Asp Glu Leu Ile Asn Ala Asp Glu Val Phe Cys Thr Gly Thr Ala
 130 135 140
 Val Val Val Ser Pro Val Gly Ser Val Thr Tyr Met Gly Lys Arg Val
 145 150 155 160
 Glu Tyr Gly Asn Gln Gly Val Gly Val Val Ser Gln Gln Leu Tyr Lys
 165 170 175
 Ser Leu Thr Ser Leu Gln Met Gly Asn Val Glu Asp Trp Met Gly Trp
 180 185 190
 Thr Met Gln Leu Asn Gln
 195

<210> 12
 <211> 445
 <212> DNA
 <213> Zea mays

<220>
 <221> unsure
 <222> (252)

<220>
 <221> unsure
 <222> (311)

<220>
 <221> unsure
 <222> (336)

10027450.12001

<220>
<221> unsure
<222> (356)

<220>
<221> unsure
<222> (361)

<220>
<221> unsure
<222> (369)

<220>
<221> unsure
<222> (384)

<220>
<221> unsure
<222> (393)

<220>
<221> unsure
<222> (418)

<220>
<221> unsure
<222> (431)

<220>
<221> unsure
<222> (437)

<400> 12
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acgcgcaaga gcgtcatcga gctcgccagg gaccgcggat acaagggttga ggaacgcctg 120
gtttccatcg acgatctggt ggccgcagac gaggtgttct gcaccgggac cgcggtggtg 180
gttgctcccg tgtcgacagt cacgtaccag ggcgagaggt atgagttcag aacggggccg 240
gacacggtgt cncaggagct gtacacgacg ctgacatcca ttcagatggg catggccgcc 300
gaggacagca ngggatggac agtaccagta gaganatta ataagggttg ggaatncatc 360
nccacaacnt tgtttccaca tcantattgt canccggtaa aatgcatact cggttatnac 420
atatgtgtgt ngcacanttg aaaaaa 445

<210> 13
<211> 115
<212> PRT
<213> Zea mays

<220>
<221> UNSURE
<222> (104)

<220>
<221> UNSURE
<222> (112)

<400> 13
Val Val Lys Gly Gly Val Val Ala Thr Pro Asp Thr Arg Gly Thr Ile
1 5 10 15
Leu Pro Gly Ile Thr Arg Lys Ser Val Ile Glu Leu Ala Arg Asp Arg
20 25 30
Gly Tyr Lys Val Glu Glu Arg Leu Val Ser Ile Asp Asp Leu Val Ala
35 40 45

Ala Asp Glu Val Phe Cys Thr Gly Thr Ala Val Val Val Ala Pro Val
 50 55 60

Ser Thr Val Thr Tyr Gln Gly Glu Arg Tyr Glu Phe Arg Thr Gly Pro
 65 70 75 80

Asp Thr Val Ser Gln Glu Leu Tyr Thr Thr Leu Thr Ser Ile Gln Met
 85 90 95

Gly Met Ala Ala Glu Asp Ser Xaa Gly Trp Thr Val Pro Val Glu Xaa
 100 105 110

Ile Asn Lys
 115

<210> 14
 <211> 1086
 <212> DNA
 <213> Oryza sativa

<400> 14
 gcacgagggc atactcagcc gctacggcaa catcgagctc agcccctcct ccggcgctcat 60
 caactacggc caggggctct tcgaggggtct gaaggcggtac agggcgggcga accaacaggg 120
 gtcgtacatg ctgttcgggc cggaggagaa cgcgcggcgg atgcagcacg gcgccgagcg 180
 catgtgcatg ccgtcgccgt cgggtggagca gttcgtccac gccgtcaagc agaccgtcct 240
 cgccaaccgc cgctgggtgc caccgcaagg aaagggggcg ctgtacatca ggccgctgct 300
 catcgggagc ggaccgattc tggggctggc tcccgccccg gactacacgt tcctcatcta 360
 cgccgcaccg gttggaacgt acttcaagga gggcttagcg ccgataaacc ttgtcgtaga 420
 ggactcgata caccggggcca tgccggggcg caccgggtggg gtcaagacga tcaccaacta 480
 cgcgcgggtg ctcaaggcgc agatggacgc caagagcata gggttcactg acgtgctgta 540
 cctcgacgcg gtgcacaaga cgtacctgga ggaggcctcc tcttgcaacc tcttcactgt 600
 caaggacggc gtcgtcgcca cgccggccac cgtgggaacc atcctgccg ggatcacgcg 660
 caagagcgtc atcgagctcg ccagggaccg cggctatcag gttgaagaac ggctcgtctc 720
 catcgacgat ctggtcggcg cagacgaggt gttctgcacc ggaacagcgg tggctcgttg 780
 cccagtatcg agtggtactt accatgggca aaggtagcag ttcaggactg gacatgacac 840
 gttatcgtag acactgcaca cgactctgac gtccatccag atgggcctgg ctgaggacaa 900
 gaaaggatgg acagtggcaa tagattaagg atggattatg ggcaaaggga tcccgattat 960
 tcctcatgtc atccaatgta gattattgtc gttttatata tcttctgtga gcgacagtga 1020
 tcacagcgca agtggaattt ggacgaacag gaagcaaagt cagatcatct tactgcgtaa 1080
 aaaaaa 1086

<210> 15
 <211> 307
 <212> PRT
 <213> Oryza sativa

<400> 15
 Glu Gly Ile Leu Ser Arg Tyr Gly Asn Ile Glu Leu Ser Pro Ser Ser
 1 5 10 15

Gly Val Ile Asn Tyr Gly Gln Gly Leu Phe Glu Gly Leu Lys Ala Tyr
 20 25 30

Arg Ala Ala Asn Gln Gln Gly Ser Tyr Met Leu Phe Arg Pro Glu Glu
 35 40 45

Asn Ala Arg Arg Met Gln His Gly Ala Glu Arg Met Cys Met Pro Ser
 50 55 60

Pro Ser Val Glu Gln Phe Val His Ala Val Lys Gln Thr Val Leu Ala
 65 70 75 80

Asn Arg Arg Trp Val Pro Pro Gln Gly Lys Gly Ala Leu Tyr Ile Arg
 85 90 95

Pro Leu Leu Ile Gly Ser Gly Pro Ile Leu Gly Leu Ala Pro Ala Pro
100 105 110

Glu Tyr Thr Phe Leu Ile Tyr Ala Ala Pro Val Gly Thr Tyr Phe Lys
115 120 125

Glu Gly Leu Ala Pro Ile Asn Leu Val Val Glu Asp Ser Ile His Arg
130 135 140

Ala Met Pro Gly Gly Thr Gly Gly Val Lys Thr Ile Thr Asn Tyr Ala
145 150 155 160

Pro Val Leu Lys Ala Gln Met Asp Ala Lys Ser Ile Gly Phe Thr Asp
165 170 175

Val Leu Tyr Leu Asp Ala Val His Lys Thr Tyr Leu Glu Glu Ala Ser
180 185 190

Ser Cys Asn Leu Phe Ile Val Lys Asp Gly Val Val Ala Thr Pro Ala
195 200 205

Thr Val Gly Thr Ile Leu Pro Gly Ile Thr Arg Lys Ser Val Ile Glu
210 215 220

Leu Ala Arg Asp Arg Gly Tyr Gln Val Glu Glu Arg Leu Val Ser Ile
225 230 235 240

Asp Asp Leu Val Gly Ala Asp Glu Val Phe Cys Thr Gly Thr Ala Val
245 250 255

Val Val Ala Pro Val Ser Ser Val Thr Tyr His Gly Gln Arg Tyr Glu
260 265 270

Phe Arg Thr Gly His Asp Thr Leu Ser Gln Thr Leu His Thr Thr Leu
275 280 285

Thr Ser Ile Gln Met Gly Leu Ala Glu Asp Lys Lys Gly Trp Thr Val
290 295 300

Ala Ile Asp
305

<210> 16
<211> 965
<212> DNA
<213> Glycine max

<400> 16
catccttggt tgtccatgct cccgagttgt gaatatcagg gactgcctca gtcctccat 60
tgactttcct tggagttgta agcccagctt agaagaggct acgctgatgt ccattttcta 120
aagtttaatt tcaactccca atatcacaag tttatataga tatatgcttt tttgaaagag 180
gctcgtgccg aattcggcac gaggaatatg gagagcattc gactaattta cccgatctgc 240
ccctctagac attcttcctt tcttctctct catcaatctc ccttcctatg cgaaccttct 300
ctctctctca agcttcgaaa gcagtttctt ctcaactcgc agaatgttct ggaagccgcc 360
tctcctctca ggccttcgcg cactctgtct tctgatccct acagtgcagc gattgaatta 420
gctgatatag aatgggacaa ccttgggttt gggcttcaac ccactgatta tatgtatata 480
atgaaatgca cacgaggtgg aaccttttcc aaaggtgaat tgcagcgttt tgggaacatc 540
gagttgaacc cctccgctgg agtttttaaac tatggccagg gattatttga gggtttgaaa 600
gcataccgca aacaagatgg gagtatactc ctcttcgctc cggaagaaaa tggtttgccg 660
atgcagatag gtgcggagcg gatgtgcata ccatcaccta ctatggagca gtttgtggaa 720
gctgtgaagg atactgtttt agctaacaaa cggtgggttc cccctgcagg taaagggtcc 780
ttgtatatta gacctttgtt aatgggaagt ggacctgtac ttggtgttgc acctgcacca 840
gagtacacat ttctaataata tgtttcacct gttgggaact acttcaagga aggtttggcc 900
ccaatcaatt tgattgtaga aaatgaattc catcgtgcaa ctctggtgg cactggagct 960
cgtgc 965

<210> 17
 <211> 252
 <212> PRT
 <213> Glycine max

<400> 17
 Met Glu Ser Ile Arg Leu Ile Tyr Pro Ile Cys Pro Ser Arg His Ser
 1 5 10 15
 Ser Phe Leu Leu Ser His Gln Ser Pro Phe Leu Cys Glu Pro Ser Leu
 20 25 30
 Ser Leu Lys Leu Arg Lys Gln Phe Pro Leu Thr Ser Gln Asn Val Leu
 35 40 45
 Glu Ala Ala Ser Pro Leu Arg Pro Ser Ala Thr Leu Ser Ser Asp Pro
 50 55 60
 Tyr Ser Glu Thr Ile Glu Leu Ala Asp Ile Glu Trp Asp Asn Leu Gly
 65 70 75 80
 Phe Gly Leu Gln Pro Thr Asp Tyr Met Tyr Ile Met Lys Cys Thr Arg
 85 90 95
 Gly Gly Thr Phe Ser Lys Gly Glu Leu Gln Arg Phe Gly Asn Ile Glu
 100 105 110
 Leu Asn Pro Ser Ala Gly Val Leu Asn Tyr Gly Gln Gly Leu Phe Glu
 115 120 125
 Gly Leu Lys Ala Tyr Arg Lys Gln Asp Gly Ser Ile Leu Leu Phe Arg
 130 135 140
 Pro Glu Glu Asn Gly Leu Arg Met Gln Ile Gly Ala Glu Arg Met Cys
 145 150 155 160
 Met Pro Ser Pro Thr Met Glu Gln Phe Val Glu Ala Val Lys Asp Thr
 165 170 175
 Val Leu Ala Asn Lys Arg Trp Val Pro Pro Ala Gly Lys Gly Ser Leu
 180 185 190
 Tyr Ile Arg Pro Leu Leu Met Gly Ser Gly Pro Val Leu Gly Val Ala
 195 200 205
 Pro Ala Pro Glu Tyr Thr Phe Leu Ile Tyr Val Ser Pro Val Gly Asn
 210 215 220
 Tyr Phe Lys Glu Gly Leu Ala Pro Ile Asn Leu Ile Val Glu Asn Glu
 225 230 235 240
 Phe His Arg Ala Thr Pro Gly Gly Thr Gly Ala Arg
 245 250

<210> 18
 <211> 1501
 <212> DNA
 <213> Triticum aestivum

<400> 18
 gcacgagccg cgcggcacgt cgggtctcccc cagccccagg ccgcatccgg gcctaccctc 60
 gcaacccatt cagaagcgat tgtccggcag cgccgtctcc gtctccaggc gaggaactgc 120
 ggcaaggagc agcccgtgtt ccgcccgtgat gacggcatca tacaacacag gaactccgga 180
 cctagtcgac ttcgactggg agactcttgg atttcaactg gtcccgcagg actttatgta 240
 tataatgaaa tgttcgtcag atgggggtgtt caccaagggt gaattgggtc catatgggcc 300
 aatcgagctg aaccctgctg ctgcagtttt aaattatggc cagggtattgc tcgaagggtc 360

tagagcacac	agaaaggagg	atgggttcagt	agttgttttt	cgccccaagg	aaaacgcgtt	420
gcggatgagg	ataggtgcag	atcggctatg	catgcctgca	ccaagcgttg	agcagttcct	480
atcagctgtc	aagcacacta	tattggcaaa	caagcgttgg	gtacccccca	ctggcaaagg	540
ttctttatat	atcaggccgc	tgctgattgg	aagtggagct	atgctaggtg	tagcacctgc	600
cccggagtat	acattttgtt	tgtatgtttg	cccagttggg	cactatttca	aggatggcct	660
gtcaccaatt	agcttattga	ctgaggaaga	atatcaccgc	gctgcacctg	gtggaactgg	720
tgatattaag	acaattggaa	attatgcttc	ggttgttagt	gctcagagaa	gagccaagga	780
gaaaggtcat	tctgatgttc	tttacttgga	tcccgtgcat	aagaagtttg	tggaggaagt	840
ttcttcctgt	aatatattga	tggatgaagga	taatgttatt	tctactccac	tattaacggg	900
aacaattcct	cctggaatca	caagaagaag	tataattgaa	attgcccaaa	atcttggaat	960
ccaggtcgaa	gagcgcctta	ttgcatagaa	tgagttgctt	gacgctgatg	aagtcttctg	1020
tacagggact	gccgttgtac	tatcacccgt	tggttccatt	gtgtaccacg	gaagaagagt	1080
ggagtatggg	ggcgggaagg	tccggagcgt	gtcccagcaa	ctgtattcgg	cacttacagc	1140
tatccagaaa	ggccttgttg	aggacagtat	gggatggagt	gtgcagttga	attagcagct	1200
tcatcatctg	gacggtctct	acgagcctcc	tccgcaagaa	aacaatgcaa	aatcacttga	1260
ccctctgtca	ggaaattttg	cagaatgtag	aatagcataa	tttccctgtg	aagatagcaa	1320
gaggtacaca	cacaacatag	catcaagctg	gatcagaaag	attaataata	atgattaaat	1380
agctgttggt	tcttctcatt	ctgtttccca	agaggactga	atgcgctttg	agtgtgaata	1440
actccataac	atacttgcaa	ttgcaaacca	tgagacataa	ataattgggtg	gcaaaaaaaaa	1500
a						1501

<210> 19
 <211> 348
 <212> PRT
 <213> Triticum aestivum

<400> 19
 Met Thr Ala Ser Tyr Asn Thr Gly Thr Pro Asp Leu Val Asp Phe Asp
 1 5 10 15
 Trp Glu Thr Leu Gly Phe Gln Leu Val Pro Thr Asp Phe Met Tyr Ile
 20 25 30
 Met Lys Cys Ser Ser Asp Gly Val Phe Thr Lys Gly Glu Leu Val Pro
 35 40 45
 Tyr Gly Pro Ile Glu Leu Asn Pro Ala Ala Ala Val Leu Asn Tyr Gly
 50 55 60
 Gln Gly Leu Leu Glu Gly Leu Arg Ala His Arg Lys Glu Asp Gly Ser
 65 70 75 80
 Val Val Val Phe Arg Pro Lys Glu Asn Ala Leu Arg Met Arg Ile Gly
 85 90 95
 Ala Asp Arg Leu Cys Met Pro Ala Pro Ser Val Glu Gln Phe Leu Ser
 100 105 110
 Ala Val Lys His Thr Ile Leu Ala Asn Lys Arg Trp Val Pro Pro Thr
 115 120 125
 Gly Lys Gly Ser Leu Tyr Ile Arg Pro Leu Leu Ile Gly Ser Gly Ala
 130 135 140
 Met Leu Gly Val Ala Pro Ala Pro Glu Tyr Thr Phe Val Val Tyr Val
 145 150 155 160
 Cys Pro Val Gly His Tyr Phe Lys Asp Gly Leu Ser Pro Ile Ser Leu
 165 170 175
 Leu Thr Glu Glu Glu Tyr His Arg Ala Ala Pro Gly Gly Thr Gly Asp
 180 185 190
 Ile Lys Thr Ile Gly Asn Tyr Ala Ser Val Val Ser Ala Gln Arg Arg
 195 200 205

Ala Lys Glu Lys Gly His Ser Asp Val Leu Tyr Leu Asp Pro Val His
210 215 220

Lys Lys Phe Val Glu Glu Val Ser Ser Cys Asn Ile Leu Met Val Lys
225 230 235 240

Asp Asn Val Ile Ser Thr Pro Leu Leu Thr Gly Thr Ile Leu Pro Gly
245 250 255

Ile Thr Arg Arg Ser Ile Ile Glu Ile Ala Gln Asn Leu Gly Ile Gln
260 265 270

Val Glu Glu Arg Leu Ile Ala Ile Asp Glu Leu Leu Asp Ala Asp Glu
275 280 285

Val Phe Cys Thr Gly Thr Ala Val Val Leu Ser Pro Val Gly Ser Ile
290 295 300

Val Tyr His Gly Arg Arg Val Glu Tyr Gly Gly Gly Lys Val Gly Ala
305 310 315 320

Val Ser Gln Gln Leu Tyr Ser Ala Leu Thr Ala Ile Gln Lys Gly Leu
325 330 335

Val Glu Asp Ser Met Gly Trp Ser Val Gln Leu Asn
340 345

<210> 20
<211> 363
<212> PRT
<213> Bacillus subtilis

<400> 20
Met Thr Lys Gln Thr Ile Arg Val Glu Leu Thr Ser Thr Lys Lys Pro
1 5 10 15

Lys Pro Asp Pro Asn Gln Leu Ser Phe Gly Arg Val Phe Thr Asp His
20 25 30

Met Phe Val Met Asp Tyr Ala Ala Asp Lys Gly Trp Tyr Asp Pro Arg
35 40 45

Ile Ile Pro Tyr Gln Pro Leu Ser Met Asp Pro Thr Ala Met Val Tyr
50 55 60

His Tyr Gly Gln Thr Val Phe Glu Gly Leu Lys Ala Tyr Val Ser Glu
65 70 75 80

Asp Asp His Val Leu Leu Phe Arg Pro Glu Lys Asn Met Glu Arg Leu
85 90 95

Asn Gln Ser Asn Asp Arg Leu Cys Ile Pro Gln Ile Asp Glu Glu Gln
100 105 110

Val Leu Glu Gly Leu Lys Gln Leu Val Ala Ile Asp Lys Asp Trp Ile
115 120 125

Pro Asn Ala Glu Gly Thr Ser Leu Tyr Ile Arg Pro Phe Ile Ile Ala
130 135 140

Thr Glu Pro Phe Leu Gly Val Ala Ala Ser His Thr Tyr Lys Leu Leu
145 150 155 160

Ile Ile Leu Ser Pro Val Gly Ser Tyr Tyr Lys Glu Gly Ile Lys Pro
165 170 175

Val Lys Ile Ala Val Glu Ser Glu Phe Val Arg Ala Val Lys Gly Gly
180 185 190

Thr Gly Asn Ala Lys Thr Ala Gly Asn Tyr Ala Ser Ser Leu Lys Ala
195 200 205

Gln Gln Val Ala Glu Glu Lys Gly Phe Ser Gln Val Leu Trp Leu Asp
210 215 220

Gly Ile Glu Lys Lys Tyr Ile Glu Glu Val Gly Ser Met Asn Ile Phe
225 230 235 240

Phe Lys Ile Asn Gly Glu Ile Val Thr Pro Met Leu Asn Gly Ser Ile
245 250 255

Leu Glu Gly Ile Thr Arg Asn Ser Val Ile Ala Leu Leu Lys His Trp
260 265 270

Gly Leu Gln Val Ser Glu Arg Lys Ile Ala Ile Asp Glu Val Ile Gln
275 280 285

Ala His Lys Asp Gly Ile Leu Glu Glu Ala Phe Gly Thr Gly Thr Ala
290 295 300

Ala Val Ile Ser Pro Val Gly Glu Leu Ile Trp Gln Asp Glu Thr Leu
305 310 315 320

Ser Ile Asn Asn Gly Glu Thr Gly Glu Ile Ala Lys Lys Leu Tyr Asp
325 330 335

Thr Ile Thr Gly Ile Gln Lys Gly Ala Val Ala Asp Glu Phe Gly Trp
340 345 350

Thr Thr Glu Val Ala Ala Leu Thr Glu Ser Lys
355 360

<210> 21
<211> 1162
<212> DNA
<213> Glycine max

<400> 21
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atcctcgtcc agatgacggc ggcgtccaac tgccggaggg ggtccatccg ctactggctc 120
agcgcggcg gcggcgactt cctcctgtcc tccgcgggct gcgccgggcc ggcgttctac 180
gccgtcgtca tcccgaccga ctactcccag tgccgccacg gcgtgcgcgc ggtgaccacg 240
tcggtgcccga tgaagccgcc gctgttcgcc accatgaaga acgtcaacta cctccccaac 300
gtgctgtcca tcatggacgc cgaggaccgc ggcgcgttcg cgtcgggtgtg ggtggacggc 360
gagggcaacg tcgccgaggg gcccatgggtg aacgtggcgt tcgtcacggc cgccggcgag 420
ctggtgctcc cggcgttcga caagatcctc gccgggtgca ccgccaagcg gctgctcgcg 480
ctggcgccga ggctggtgga gtccggcctc ctcaaggccg tcaccacccg ccacatcgcc 540
gccgacgagg ccaagcgctg ctccgcccag atggcggttcg tcggcagcgg cctccccgtc 600
ctgcccacatg tcgagtggga cgaccagctc atcggcgacg ggaagggtgg gaagacgatg 660
atggcgctgt cggatctgct ctgggaggac atgaaatcgg ggccggacag gatcgagtc 720
ccgtacaagt gatggattat tggagttggg tgaggctcct cgggcgtacg tcagaaagag 780
gtgtgctacc gacgtgtgga ttcacgacgg taagcttcac ctgttaggga ttcacgtctc 840
ttcgacttta tatgagagga gctacgtcca tcggagatag gaggagaagg gcaacgtgcc 900
gagtatatat gtgtagtgtg cgtacgcgtg agcagagctga gatggatatg atgcagtatc 960
gtgtcgtttc gtttcgtttc tccttgtgtt catgtgtggc ttgtatgggt ttttatctgt 1020
acgtgtcgtc aacgtaatcc ttgtattttg cgggtgtatca gtactgtatg agtgtatgtg 1080
tttatcgatt gatcattaag tgaatgaata atggattctc tcgatttcaa atgtaaaaaa 1140
aaaaaaaaaa aaaaaaaaaa aa 1162

<210> 22
<211> 243

<212> PRT
<213> Glycine max

<400> 22

Ala Arg Val Gln Pro Lys Ala Arg Ile Gly Thr Pro Phe Pro Arg Asp
1 5 10 15
Thr Leu Arg Ser Ile Leu Val Gln Met Thr Ala Ala Ser Asn Cys Arg
20 25 30
Arg Gly Ser Ile Arg Tyr Trp Leu Ser Ala Gly Gly Gly Asp Phe Leu
35 40 45
Leu Ser Ser Ala Gly Cys Ala Gly Pro Ala Phe Tyr Ala Val Val Ile
50 55 60
Pro Thr Asp Tyr Ser Gln Cys Arg His Gly Val Arg Ala Val Thr Thr
65 70 75 80
Ser Val Pro Met Lys Pro Pro Leu Phe Ala Thr Met Lys Asn Val Asn
85 90 95
Tyr Leu Pro Asn Val Leu Ser Ile Met Asp Ala Glu Asp Arg Gly Ala
100 105 110
Phe Ala Ser Val Trp Val Asp Gly Glu Gly Asn Val Ala Glu Gly Pro
115 120 125
Met Val Asn Val Ala Phe Val Thr Ala Ala Gly Glu Leu Val Leu Pro
130 135 140
Ala Phe Asp Lys Ile Leu Ala Gly Cys Thr Ala Lys Arg Leu Leu Ala
145 150 155 160
Leu Ala Pro Arg Leu Val Glu Ser Gly Leu Leu Lys Ala Val Thr Thr
165 170 175
Arg His Ile Ala Ala Asp Glu Ala Lys Arg Cys Ser Ala Glu Met Ala
180 185 190
Phe Val Gly Ser Gly Leu Pro Val Leu Pro Ile Val Glu Trp Asp Asp
195 200 205
Gln Leu Ile Gly Asp Gly Lys Val Gly Lys Thr Met Met Ala Leu Ser
210 215 220
Asp Leu Leu Trp Glu Asp Met Lys Ser Gly Pro Asp Arg Ile Ala Val
225 230 235 240

Pro Tyr Lys

<210> 23
<211> 1045
<212> DNA
<213> Glycine max

<400> 23

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<210> 24
 <211> 285
 <212> PRT
 <213> Glycine max.

<400> 24
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 His Gly Val Phe Asp Thr Ala Ala Ile Met Asp Gly Tyr Leu Tyr Glu
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 Leu Asp Gln His Leu Asp Arg Phe Leu Arg Ser Ala Ser Met Ser Lys
 35 40 45
 Ile Asp Pro Pro Phe Asp Arg Gly Ser Ile Arg Arg Ile Leu Ile Gln
 50 55 50
 Thr Val Ser Ala Ser Lys Cys Arg Lys Gly Ser Leu Arg Tyr Trp Leu
 65 70 75 80
 Ser Ala Gly Pro Gly Asp Phe Gln Leu Ser Pro Ser Cys Cys His Arg
 85 90 95
 Ser Ser Leu Tyr Ala Ile Val Ile Gln Asp Leu Ser Pro Ser Ser Pro
 100 105 110
 Asn Phe Arg Gly Val Lys Val Val Thr Ser Ser Ile Pro Ile Lys His
 115 120 125
 Pro Lys Phe Ala Ile Thr Lys Ser Val Asn Tyr Leu Pro Asn Val Leu
 130 135 140
 Ser Lys Val Glu Ala Glu Glu Ala Gly Ala Phe Val Gly Ile Trp Leu
 145 150 155 160
 Asp Gly Glu Gly Phe Val Ala Glu Gly Pro Asn Met Asn Val Ala Phe
 165 170 175
 Val Thr Lys Asp Lys Glu Leu Ile Met Pro His Phe Asp Lys Ile Leu
 180 185 190
 Ser Gly Cys Thr Ala Lys Arg Val Leu Thr Leu Ala Glu Ser Leu Leu
 195 200 205
 Arg Glu Gly Lys Leu Lys Gly Ile Arg Val Lys Thr Val Thr Val Glu
 210 215 220
 Glu Gly Lys Gln Ala Asp Glu Met Met Leu Leu Gly Ser Gly Val Leu
 225 230 235 240
 Val Cys Pro Val Val Gln Trp Asp Glu Gln Val Ile Gly Asp Gly Lys
 245 250 255

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Glu Gly Pro Ile Thr Gln Ala Leu Leu Asn Leu Ile Val Glu Asp Met
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<212> DNA
<213> Oryza sativa

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aaa 1323

<210> 26
<211> 297
<212> PRT
<213> Oryza sativa

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Asp Thr Ala Ile Val Leu Asp Gly Tyr Leu Tyr Glu Leu Asp Val His
35 40 45
Leu Asp Arg Phe Leu Ser Ser Ala Ser Lys Ala Lys Ile Ser Ser Pro
50 55 60
Phe Ser Arg Ser Val Leu His Ser Ile Leu Ile Gln Leu Thr Ala Ala
65 70 75 80
Ser Lys Cys Lys Lys Gly Thr Leu Arg Tyr Trp Leu Ser Ala Gly Pro
85 90 95
Gly Asp Phe Leu Leu Ser Ser Ala Gly Cys Pro Thr Ser Ala Phe Tyr
100 105 110
Ala Val Val Ile Asp Gln Asp Val Ser Gln Cys Lys Glu Gly Val Lys
115 120 125

Val Ile Thr Ser Asn Ile Pro Met Lys Pro Ser Leu Phe Ala Thr Ala
130 135 140

Lys Asn Val Asn Tyr Leu Pro Asn Val Leu Ser Val Met Glu Ala Glu
145 150 155 160

Glu Lys Gly Ala Ser Ser Ser Ile Trp Val Asp Glu Glu Gly Tyr Ile
165 170 175

Ala Glu Gly Pro Asn Val Asn Val Ala Phe Ile Thr Gln Asp Lys Glu
180 185 190

Leu Val Met Pro Pro Phe Asp Asn Ile Leu His Gly Cys Thr Ala Lys
195 200 205

Arg Leu Leu Glu Leu Ala Pro Lys Leu Val Asp Gln Gly Leu Leu Lys
210 215 220

Gly Val Ala Thr Lys Lys Leu Thr Val Glu Glu Ala Lys Ala Ala Ala
225 230 235 240

Glu Met Met Tyr Val Gly Ser Thr Leu Pro Leu Leu Pro Ile Ile Val
245 250 255

Trp Asp Asp Gln Pro Ile Gly Asn Gly Arg Val Gly Glu Leu Thr Met
260 265 270

Leu Leu Ser Asp Met Leu Trp Asp Asp Met Val Ala Gly Pro Gly Thr
275 280 285

Gln Arg Ile Pro Val Pro Tyr Val Glu
290 295

<210> 27
<211> 542
<212> DNA
<213> Triticum aestivum

<400> 27
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tt 542

<210> 28
<211> 180
<212> PRT
<213> Triticum aestivum

<400> 28
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20 25 30

Thr Ser Ser Ile Pro Ile Lys Ser Pro Gln Phe Ala Val Met Lys Ser
35 40 45

Val Asn Tyr Leu Pro Asn Ala Leu Thr Lys Val Glu Gly Glu Glu Asn
50 55 60

Gly Ala Phe Thr Gly Ile Trp Leu Asp Asp Glu Gly Phe Val Ala Glu
65 70 75 80

Gly Ser Asn Met Asn Val Gly Phe Val Thr Lys Asn Lys Glu Leu Leu
85 90 95

Met Pro Arg Phe Asp Lys Ile Leu Ser Gly Cys Thr Ala Arg Arg Val
100 105 110

Leu Thr Leu Ala Glu His Leu Val Ala His Gly Lys Leu Ser Arg Val
115 120 125

Ile Ser Arg Asn Val Ser Val Glu Glu Gly Lys Met Ala Asp Glu Met
130 135 140

Met Leu Ile Gly Ser Gly Ile Leu Val Lys Pro Val Val Gln Trp Asp
145 150 155 160

Asp Lys Ile Ile Gly Ser Gly Gln Glu Gly Pro Ile Ala Gln Ala Leu
165 170 175

Tyr Asp Leu Ile
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<210> 29
<211> 288
<212> PRT
<213> Methanococcus jannaschii

<400> 29
Met Lys Ile Tyr Leu Asn Gly Lys Phe Val Asp Glu Lys Asp Ala Lys
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Val Ser Val Phe Asp His Gly Leu Leu Tyr Gly Asp Gly Val Phe Glu
20 25 30

Gly Ile Arg Ala Tyr Asp Gly Val Val Phe Met Leu Lys Glu His Ile
35 40 45

Asp Arg Leu Tyr Asp Ser Ala Lys Ser Leu Cys Ile Asp Ile Pro Leu
50 55 60

Thr Lys Glu Glu Met Ile Asp Val Val Leu Glu Thr Leu Arg Val Asn
65 70 75 80

Asn Leu Arg Asp Ala Tyr Ile Arg Leu Val Val Thr Arg Gly Val Gly
85 90 95

Asp Leu Gly Leu Asp Pro Arg Lys Cys Gly Lys Pro Thr Ile Phe Cys
100 105 110

Ile Ala Ile Pro Met Pro Pro Leu Leu Gly Glu Asp Gly Ile Arg Ala
115 120 125

Ile Thr Val Ser Val Arg Arg Leu Pro Val Asp Val Leu Asn Pro Ala
130 135 140

Val Lys Ser Leu Asn Tyr Leu Asn Ser Val Leu Ala Lys Ile Gln Ala
145 150 155 160

Asn Tyr Ala Gly Val Asp Glu Ala Phe Leu Leu Asp Asp Lys Gly Phe
165 170 175

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Val Val Glu Gly Thr Gly Asp Asn Ile Phe Ile Val Lys Asn Gly Val
180 185 190

Leu Lys Thr Pro Pro Val Tyr Gln Ser Ile Leu Lys Gly Ile Thr Arg
195 200 205

Asp Val Val Ile Lys Leu Ala Lys Glu Glu Gly Ile Glu Val Val Glu
210 215 220

Glu Pro Leu Thr Leu His Asp Leu Tyr Thr Ala Asp Glu Leu Phe Ile
225 230 235 240

Thr Gly Thr Ala Ala Glu Ile Val Pro Val Phe Glu Ile Asp Gly Arg
245 250 255

Val Ile Asn Asn Lys Gln Val Gly Glu Ile Thr Lys Lys Leu Lys Glu
260 265 270

Lys Phe Lys Asp Ile Arg Thr Lys Trp Gly Ile Lys Val Tyr Asp Glu
275 280 285

<210> 30
<211> 1062
<212> DNA
<213> Zea mays

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<210> 31
<211> 310
<212> PRT
<213> Zea mays

<400> 31
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Ile Leu Val Trp Val Gly Asp Glu Leu Leu Pro Arg Asn Ser Ala Lys
20 25 30

Val Ser Val Phe Asp Ser Val Val Gln Gly Gly Asp Ala Val Trp Glu
35 40 45

Gly Leu Arg Ile Tyr Asp Gly Lys Val Phe Lys Leu Asp Glu His Leu
50 55 60

Asp Arg Leu Phe Asp Ser Ala Lys Ala Met Ala Phe Ser Asn Val Pro
65 70 75 80

Thr Arg Asp Trp Ile Lys Asp Ala Ile Phe Lys Thr Leu Ile Ala Asn
85 90 95

Gly Met Phe Asn Asn Ala His Ile Arg Leu Thr Leu Thr Arg Gly Lys
100 105 110

Lys Val Thr Ser Gly Met Ser Pro Ala Phe Asn Leu Tyr Gly Cys Ala
115 120 125

Leu Ile Val Leu Ala Glu Trp Lys Pro Pro Val Tyr Asp Asn Ser His
130 135 140

Gly Ile Lys Leu Val Thr Ala Thr Thr Arg Arg Asn Ser Pro Asn Ser
145 150 155 160

Ile Asp Pro Lys Ile His His Asn Asn Leu Ile Asn Asn Ile Leu Ala
165 170 175

Lys Ile Glu Gly Asn Leu Ala Gln Ala Glu Asp Ala Ile Met Leu Asp
180 185 190

Lys Asp Gly Phe Val Ser Glu Thr Asn Ala Thr Asn Ile Phe Met Val
195 200 205

Lys Lys Gly Ile Val Leu Thr Pro His Ala Asp Tyr Cys Leu Pro Gly
210 215 220

Ile Thr Arg Ala Thr Val Met Asp Leu Val Val Lys Glu Asn Phe Val
225 230 235 240

Leu His Glu Arg Arg Ile Ser Leu Ser Glu Phe His Ala Ala Asp Glu
245 250 255

Val Trp Thr Thr Gly Thr Met Gly Glu Ile Thr Pro Val Val Met Ile
260 265 270

Asp Gly Arg Glu Ile Gly Asp Gly Lys Ile Gly Pro Val Thr Arg Gln
275 280 285

Ile Gln Lys Ala Tyr Lys Ile Leu Thr Ala Gly Gln Gly Val Pro Ile
290 295 300

Pro Gly Val Ala Glu Val
305 310

<210> 32
<211> 1186
<212> DNA
<213> Triticum aestivum

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aaaccaccag tttatgataa ctacatggg ataaagttgg taactgccgc cacacgtcgt 300
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<210> 33
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 <212> PRT
 <213> *Triticum aestivum*

<400> 33
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 20 25 30
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 35 40 45
 Ile Arg Leu Thr Leu Thr Arg Gly Lys Lys Val Thr Ser Gly Met Ser
 50 55 60
 Pro Thr Phe Asn Leu Tyr Gly Cys Val Leu Ile Val Leu Ala Glu Trp
 65 70 75 80
 Lys Pro Pro Val Tyr Asp Asn Ser His Gly Ile Lys Leu Val Thr Ala
 85 90 95
 Ala Thr Arg Arg Asn Ser Pro Asn Ser Val Asp Ser Lys Ile His His
 100 105 110
 Asn Asn Leu Ile Asn Asn Ile Leu Ala Lys Ile Glu Gly Asn Leu Ala
 115 120 125
 Gln Ala Glu Asp Ala Ile Met Leu Asp Gln Asp Gly Phe Val Ser Glu
 130 135 140
 Thr Asn Ala Thr Asn Ile Phe Met Val Lys Lys Gly Ile Val Leu Thr
 145 150 155 160
 Pro His Ala Asp Tyr Cys Leu Pro Gly Ile Thr Arg Ala Thr Val Lys
 165 170 175
 Asp Leu Val Val Lys Glu Asn Leu Val Leu His Glu Arg Arg Ile Ser
 180 185 190
 Leu Ser Glu Phe His Ala Ala Asp Glu Val Trp Thr Thr Gly Thr Met
 195 200 205
 Gly Glu Ile Thr Pro Val Val Met Ile Asp Gly Arg Glu Ile Gly Asp
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 Gly Lys Ile Gly Leu Val Thr Arg Gln Ile Gln Ser Ala Tyr Lys Val
 225 230 235 240
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 245 250 255

<210> 34
 <211> 210
 <212> PRT
 <213> *Escherichia coli*

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 His Asp Ser Ala Lys Tyr Arg Val Ser Ser Asp Met Ala Cys Arg Asp
 50 55 60
 Val Arg Lys Asn Asn Thr Ser Ala Tyr Arg Val Gly Asp Val Gly Met
 65 70 75 80
 Gly Val Asn Ala Gly Tyr Ser Thr Asp Val Ala Ala Trp Gly Ala Tyr
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 Gly Ala Ala Gly Asp Ala Met Val Ser Ser Trp Asn Arg Ala Ala Asn
 100 105 110
 Thr Thr Ala Ala Lys Ala Gly Gly Asn Tyr Ser Ser Val Gly Ser Ala
 115 120 125
 Arg Arg His Gly Tyr Gly Ala Asp Val Asn Gly Tyr Ser Gly Ala Gly
 130 135 140
 Asn Val Lys Asp Gly Val Thr Thr Ser Ser Ala Gly Thr Arg Asp Ala
 145 150 155 160
 Lys Ala Lys Gly Val Arg Val Ser Arg Ser Tyr Ala Asp Val Met Ser
 165 170 175
 Gly Thr Ala Ala Thr Val Arg Ser Val Asp Gly Val Gly Gly Arg Cys
 180 185 190
 Gly Val Thr Lys Arg Ala Gly Thr Gly Thr Asp Lys Trp Gly Trp Asp
 195 200 205
 Val Asn
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<210> 35
 <211> 1626
 <212> DNA
 <213> Zea mays

<400> 35
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 gaggaacttc ttgctgccgc aaaggtgttc ttagcctcgg gaaagaaggt taaagttccc 960
 acattccttg tcctgccac acaaaagggtg tggatggacg tatatagcct tcctgtacca 1020

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<210> 36
 <211> 428
 <212> PRT
 <213> Zea mays

<400> 36

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			20					25					30		
Phe	Gly	Glu	Asp	Ala	Lys	Val	Trp	Asp	Arg	Glu	Lys	Val	Val	Ile	Ile
		35					40					45			
Pro	Asp	His	Tyr	Ile	Phe	Thr	Ser	Asp	Glu	Arg	Ala	Asn	Arg	Asn	Val
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Asp	Ile	Leu	Arg	Asp	Phe	Cys	Leu	Glu	Gln	Asn	Ile	Lys	Tyr	Phe	Tyr
65					70					75					80
Asp	Ile	Lys	Asp	Leu	Ser	Asp	Phe	Arg	Ala	Asn	Pro	Asp	Tyr	Lys	Gly
			85					90						95	
Val	Cys	His	Ile	Ala	Leu	Ala	Gln	Glu	Gly	His	Cys	Arg	Pro	Gly	Glu
			100					105					110		
Val	Leu	Leu	Gly	Thr	Asp	Ser	His	Thr	Cys	Asn	Ala	Gly	Ala	Phe	Gly
		115					120					125			
Gln	Phe	Ala	Thr	Gly	Ile	Gly	Asn	Thr	Asp	Ala	Gly	Phe	Val	Met	Gly
		130				135					140				
Thr	Gly	Lys	Ala	Leu	Leu	Lys	Val	Pro	Pro	Thr	Ile	Arg	Phe	Val	Leu
145					150					155					160
Asp	Gly	Glu	Met	Pro	Pro	Tyr	Leu	Leu	Ala	Lys	Asp	Leu	Ile	Leu	Gln
				165					170					175	
Ile	Ile	Gly	Glu	Ile	Ser	Val	Ser	Gly	Ala	Thr	Tyr	Lys	Ser	Met	Glu
			180					185					190		
Phe	Val	Gly	Ser	Thr	Val	Glu	Ser	Leu	Thr	Met	Glu	Glu	Arg	Met	Thr
		195					200					205			
Leu	Cys	Asn	Met	Val	Val	Glu	Ala	Gly	Gly	Lys	Asn	Gly	Val	Val	Pro
	210					215					220				
Ala	Asp	Glu	Thr	Thr	Phe	Lys	Tyr	Leu	Glu	Gly	Arg	Thr	Ser	Val	Asp
225					230					235					240
Tyr	Gln	Pro	Val	Tyr	Ser	Asp	Ala	Glu	Ala	Arg	Phe	Phe	Ser	Asp	Tyr
				245					250					255	

10027450 "123001"

Arg Phe Asp Val Ser Lys Leu Glu Pro Val Val Ala Lys Pro His Ser
260 265 270

Pro Asp Asn Arg Ala Leu Ala Arg Glu Cys Lys Asp Val Lys Ile Asp
275 280 285

Arg Val Tyr Ile Gly Ser Cys Thr Gly Gly Lys Thr Glu Asp Phe Leu
290 295 300

Ala Ala Ala Lys Val Phe Leu Ala Ser Gly Lys Lys Val Lys Val Pro
305 310 315 320

Thr Phe Leu Val Pro Ala Thr Gln Lys Val Trp Met Asp Val Tyr Ser
325 330 335

Leu Pro Val Pro Gly Ser Gly Gly Lys Thr Cys Ala Gln Ile Phe Glu
340 345 350

Glu Ala Gly Cys Asp Thr Pro Ala Ser Pro Asn Cys Gly Ala Cys Leu
355 360 365

Gly Gly Pro Arg Asp Thr Tyr Ala Arg Met Asn Glu Pro Thr Val Cys
370 375 380

Val Ser Thr Thr Asn Arg Asn Phe Pro Gly Arg Met Gly His Lys Glu
385 390 395 400

Gly Gln Ile Tyr Leu Ala Ser Pro Tyr Thr Ala Ala Ala Ser Ala Leu
405 410 415

Thr Gly Tyr Val Thr Asp Pro Arg Asp Phe Leu Met
420 425

<210> 37
<211> 1688
<212> DNA
<213> Zea mays

<220>
<221> unsure
<222> (1673)

<400> 37

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cggttcgcga	caaggtccag	aaggagctgg	ccgcgcgcgc	gcagcgccgc	gcgggcttga	180
cccgcgggac	caagccgtgc	agcgtgcgcg	ccgtcgcttc	gcccgcgcgc	gccctgtcgt	240
ccaccggctc	ggtgaagagc	gcgatgacga	tgacggagaa	gatactggcg	cgggcgtcgc	300
agcgcgcggc	gctggagccc	ggggagaacg	tgtgggtcga	cgtcgacgtg	ctcatgacgc	360
acgacgtctg	cgggcccggc	gccttcgaca	tcttcaagaa	ggagttcggg	gaggacgcca	420
gggtctggga	ccgcgagaag	ctcgtcgtca	tcccggacca	ctacatcttc	accagcgacg	480
gccgtgccaa	acgcaacgtc	gacatcctca	gggacttctg	tgccggagcag	aacatcaagt	540
acttctatga	catcaaggac	ctcagcgatt	tcagggtctaa	tccggactac	aaaggcgtct	600
gccacatcgc	acttgctcag	gaagcccact	gcgcaccagg	cgaggttctc	ttgggcaactg	660
attctcatac	atgcaatgct	ggagcttttg	gtcagtttgc	aactggaatc	ggaaacactg	720
atgcaggttt	tgtgttgggc	actggaaagg	ctcttctcaa	ggtgccacct	actatcaggt	780
ttatattaga	tggagagatg	ccgccttatt	tacttgcgaa	ggatctgatt	ttgcaaatta	840
ttggagagat	ttcagtatct	ggtgcgacct	acaaatcaat	ggagtttggt	ggatcaactg	900
tagaaagtct	aacctatgga	gagcgtatga	cactatgcaa	catggttatt	gaagctgggtg	960
gaaagaacgg	tgttgtgcct	gctgatgaaa	ctacatttaa	ataccttgag	ggtaagacat	1020
cagtcgatta	tgaacctgtc	tacagtgatg	ctcaagccag	atcttttagc	gactaccggt	1080
ttgatgtatc	aaaactggag	ccagtagtgt	ccaagccaca	ttcgccctgac	aaccgtgctc	1140
cagcacgaga	atgcaaatg	gtgaagatcg	accgagtcta	tattggttct	tgcaactggtg	1200
gtaagaccga	ggatttcctt	gctgctgcaa	aggtgttctt	agcctcgga	aagaaggtta	1260
aagttccac	atttcttgct	cctgccacac	aaaagggtgtg	ggttgacata	tatagcctcc	1320
ctgtaccagg	atctggtggc	aaaacttgct	cccagatatt	tgaggaggct	ggttggtgaca	1380

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tgaatgaacc tactgtctgc gtgtccacca cgaacaggaa ctttccgggc aggatgggcc 1500
acaaggaagg gcaaattctac ctggcgtctc cctacactgc ggctgcctca gccctgacgg 1560
ggtatgttac ggaccccaag gacttcctca tgtaaccgtc ttgaaacaac aacagatttc 1620
atgatgtaac agagtgggtg tactgctggt tttcgtgctg aacttttgtc cangcatgtc 1680
cttcgttg 1688

<210> 38
<211> 443
<212> PRT
<213> Zea mays

<400> 38

Met Thr Met Thr Glu Lys Ile Leu Ala Arg Ala Ser Glu Arg Ala Ala
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Leu Glu Pro Gly Glu Asn Val Trp Val Asp Val Asp Val Leu Met Thr
20 25 30
His Asp Val Cys Gly Pro Gly Ala Phe Asp Ile Phe Lys Lys Glu Phe
35 40 45
Gly Glu Asp Ala Arg Val Trp Asp Arg Glu Lys Leu Val Val Ile Pro
50 55 60
Asp His Tyr Ile Phe Thr Ser Asp Gly Arg Ala Lys Arg Asn Val Asp
65 70 75 80
Ile Leu Arg Asp Phe Cys Ala Glu Gln Asn Ile Lys Tyr Phe Tyr Asp
85 90 95
Ile Lys Asp Leu Ser Asp Phe Arg Ala Asn Pro Asp Tyr Lys Gly Val
100 105 110
Cys His Ile Ala Leu Ala Gln Glu Ala His Cys Arg Pro Gly Glu Val
115 120 125
Leu Leu Gly Thr Asp Ser His Thr Cys Asn Ala Gly Ala Phe Gly Gln
130 135 140
Phe Ala Thr Gly Ile Gly Asn Thr Asp Ala Gly Phe Val Leu Gly Thr
145 150 155 160
Gly Lys Ala Leu Leu Lys Val Pro Pro Thr Ile Arg Phe Ile Leu Asp
165 170 175
Gly Glu Met Pro Pro Tyr Leu Leu Ala Lys Asp Leu Ile Leu Gln Ile
180 185 190
Ile Gly Glu Ile Ser Val Ser Gly Ala Thr Tyr Lys Ser Met Glu Phe
195 200 205
Val Gly Ser Thr Val Glu Ser Leu Thr Met Glu Glu Arg Met Thr Leu
210 215 220
Cys Asn Met Val Ile Glu Ala Gly Gly Lys Asn Gly Val Val Pro Ala
225 230 235 240
Asp Glu Thr Thr Phe Lys Tyr Leu Glu Gly Lys Thr Ser Val Asp Tyr
245 250 255
Glu Pro Val Tyr Ser Asp Ala Gln Ala Arg Phe Phe Ser Asp Tyr Arg
260 265 270
Phe Asp Val Ser Lys Leu Glu Pro Val Val Ala Lys Pro His Ser Pro
275 280 285

Asp Asn Arg Ala Pro Ala Arg Glu Cys Lys Asp Val Lys Ile Asp Arg
 290 295 300
 Val Tyr Ile Gly Ser Cys Thr Gly Gly Lys Thr Glu Asp Phe Leu Ala
 305 310 315 320
 Ala Ala Lys Val Phe Leu Ala Ser Gly Lys Lys Val Lys Val Pro Thr
 325 330 335
 Phe Leu Val Pro Ala Thr Gln Lys Val Trp Leu Asp Ile Tyr Ser Leu
 340 345 350
 Pro Val Pro Gly Ser Gly Gly Lys Thr Cys Ser Gln Ile Phe Glu Glu
 355 360 365
 Ala Gly Cys Asp Thr Pro Ala Ser Pro Asn Cys Gly Ala Cys Leu Gly
 370 375 380
 Gly Pro Arg Asp Thr Tyr Ala Arg Met Asn Glu Pro Thr Val Cys Val
 385 390 395 400
 Ser Thr Thr Asn Arg Asn Phe Pro Gly Arg Met Gly His Lys Glu Gly
 405 410 415
 Gln Ile Tyr Leu Ala Ser Pro Tyr Thr Ala Ala Ala Ser Ala Leu Thr
 420 425 430
 Gly Tyr Val Thr Asp Pro Lys Asp Phe Leu Met
 435 440

<210> 39
 <211> 512
 <212> DNA
 <213> Oryza sativa

<220>
 <221> unsure
 <222> (303)..(303)

<220>
 <221> unsure
 <222> (331)

<220>
 <221> unsure
 <222> (400)

<220>
 <221> unsure
 <222> (467)

<220>
 <221> unsure
 <222> (486)

<220>
 <221> unsure
 <222> (495)

<220>
 <221> unsure
 <222> (509)

<400> 39
 cttacagttt gccacgttgc ttttgcctcaa gaggggtcatt gcagaccagg cgaggttctc 60
 cttggtactg attctcatac atgcaatgct ggagcctttg gccaatattgc aactggaatt 120
 ggaaacactg atgctggttt tgtgatgggc actgggaagg ctcttcttaa ggtgcctcca 180
 actatcaggt ttgtattaga tggagaaatg ccaccttatt tacttgcaaa ggatctgatt 240
 ttacaaatta ttggtgagat ttctgtatct ggcgcaacat acaaatccat ggagtttgtt 300
 ggntcaactg tggaaagtct aaatatggaa nagcgaatga cactgtgcaa catggttatt 360
 gaagctggtg gcaagaatgg tgttgtgcct gcccgatcan actacattta actatcttga 420
 gggcaagaca tcagttgaat acgagcctgt catagtgatg ctcaagncaa atttgtagt 480
 gactancggt ttgangtata caaattggng ca 512

<210> 40
 <211> 127
 <212> PRT
 <213> Oryza sativa

<220>
 <221> UNSURE
 <222> (109)

<400> 40
 Val Cys His Val Ala Leu Ala Gln Glu Gly His Cys Arg Pro Gly Glu
 1 5 10 15
 Val Leu Leu Gly Thr Asp Ser His Thr Cys Asn Ala Gly Ala Phe Gly
 20 25 30
 Gln Phe Ala Thr Gly Ile Gly Asn Thr Asp Ala Gly Phe Val Met Gly
 35 40 45
 Thr Gly Lys Ala Leu Leu Lys Val Pro Pro Thr Ile Arg Phe Val Leu
 50 55 60
 Asp Gly Glu Met Pro Pro Tyr Leu Leu Ala Lys Asp Leu Ile Leu Gln
 65 70 75 80
 Ile Ile Gly Glu Ile Ser Val Ser Gly Ala Thr Tyr Lys Ser Met Glu
 85 90 95
 Phe Val Gly Ser Thr Val Glu Ser Leu Asn Met Glu Xaa Arg Met Thr
 100 105 110
 Leu Cys Asn Met Val Ile Glu Ala Gly Gly Lys Asn Gly Val Val
 115 120 125

<210> 41
 <211> 823
 <212> DNA
 <213> Glycine max

<400> 41
 cttgagggca agacatctct gccatatgaa cctgtttata gtgacgatca agcaagattt 60
 ctgcagagat atagatttga tgtctcaaaa ttggagccag tgggtggcaa gcctcattct 120
 ccggataatc gtgctttggc aagagagtgc aaggatgtga aaattgacag agtatacata 180
 ggatcttgta caggtggcaa aacagaggat ttcattggctg cagcaaaaagt ttttctggca 240
 tcaggtaaac aggtcaaagt tctacattt cttgtgcytg caacacaaaaa ggtttggatg 300
 gacttgact cctccctgt ccctggatct ggtggttaaga catgctcaca gatatttgaa 360
 gaagttgggt gtgacacacc agctagtccct agttgtggtg cttggttggg tggcccaaaa 420
 gatacttacg cacgcatgaa tgaacctaa gtttgtgttt caactacgaa cagggaacttc 480
 ccgggccgaa tgggacacaa ggaaggtcaa atctatttgg cttcccttta tacagctgct 540
 gcatctgcat tgaccgggta tgttactgat cctagagagt tcttgtagta gaattgtgtt 600
 acaatcatct cattgtgttg tactcgttgt tggttatttg tgtattctct actctctact 660
 agtcataagt taaaactgac aactatttaa gcttaacca tcttttagta tttctaagtt 720
 gatctttaga atcattcata tatgtgggtt aggtcaattc agatcaacat gaagttcaat 780
 ttcaaattta gtagtgtttg gtctttttaa aaaaaaaaaa aaa 823

<210> 42
 <211> 195
 <212> PRT
 <213> Glycine max

<220>
 <221> UNSURE
 <222> (93)

<400> 42
 Leu Glu Gly Lys Thr Ser Leu Pro Tyr Glu Pro Val Tyr Ser Asp Asp
 1 5 10 15
 Gln Ala Arg Phe Leu Ala Glu Tyr Arg Phe Asp Val Ser Lys Leu Glu
 20 25 30
 Pro Val Val Ala Lys Pro His Ser Pro Asp Asn Arg Ala Leu Ala Arg
 35 40 45
 Glu Cys Lys Asp Val Lys Ile Asp Arg Val Tyr Ile Gly Ser Cys Thr
 50 55 60
 Gly Gly Lys Thr Glu Asp Phe Met Ala Ala Ala Lys Val Phe Leu Ala
 65 70 75 80
 Ser Gly Lys Gln Val Lys Val Pro Thr Phe Leu Val Xaa Ala Thr Gln
 85 90 95
 Lys Val Trp Met Asp Leu Tyr Ser Leu Pro Val Pro Gly Ser Gly Gly
 100 105 110
 Lys Thr Cys Ser Gln Ile Phe Glu Glu Val Gly Cys Asp Thr Pro Ala
 115 120 125
 Ser Pro Ser Cys Gly Ala Cys Leu Gly Gly Pro Lys Asp Thr Tyr Ala
 130 135 140
 Arg Met Asn Glu Pro Lys Val Cys Val Ser Thr Thr Asn Arg Asn Phe
 145 150 155 160
 Pro Gly Arg Met Gly His Lys Glu Gly Gln Ile Tyr Leu Ala Ser Pro
 165 170 175
 Tyr Thr Ala Ala Ala Ser Ala Leu Thr Gly Tyr Val Thr Asp Pro Arg
 180 185 190
 Glu Phe Leu
 195

<210> 43
 <211> 530
 <212> DNA
 <213> Triticum aestivum

<400> 43
 gcacgagctt tattgctgct gcaaaggtgt tcttagcttc gggcaagaag gttaaggttc 60
 ccacttttct cggttcctgcg actcaaaagg tgtggatgga cgtgtatagt ctccccgtac 120
 caggatctgg tggcaaaaca tgctcccaga tatttgaaga ggctggttgt gatacaccag 180
 ctagtccctaa ttgtggtgct tgtttggtg gtcctcgtga tacatatgca cggatgaatg 240
 aacctacggt ctgtgtatca acgacgaaca ggaacttccc gggcaggatg ggccacaagg 300
 aagggcagat ctacctggct tctcccttca ccgcggcggc ctcagctttg acgggatatg 360
 tcacggaccc cagggacttc ctgtcgtaga gatcttgaaa acaatgaatt tgtgttgcg 420
 accgtcctgt actggtactt tttgttcgtg ttcgaaactg tagtttagat gcgtcatgtg 480
 tgtgtcgtgc tgagaaataa gctactcaac gagtagcagt tgtaactgtt 530

<210> 44
 <211> 126
 <212> PRT
 <213> Triticum aestivum

<400> 44
 Phe Ile Ala Ala Ala Lys Val Phe Leu Ala Ser Gly Lys Lys Val Lys
 1 5 10 15
 Val Pro Thr Phe Leu Val Pro Ala Thr Gln Lys Val Trp Met Asp Val
 20 25 30
 Tyr Ser Leu Pro Val Pro Gly Ser Gly Gly Lys Thr Cys Ser Gln Ile
 35 40 45
 Phe Glu Glu Ala Gly Cys Asp Thr Pro Ala Ser Pro Asn Cys Gly Ala
 50 55 60
 Cys Leu Gly Gly Pro Arg Asp Thr Tyr Ala Arg Met Asn Glu Pro Thr
 65 70 75 80
 Val Cys Val Ser Thr Thr Asn Arg Asn Phe Pro Gly Arg Met Gly His
 85 90 95
 Lys Glu Gly Gln Ile Tyr Leu Ala Ser Pro Phe Thr Ala Ala Ala Ser
 100 105 110
 Ala Leu Thr Gly Tyr Val Thr Asp Pro Arg Asp Phe Leu Ser
 115 120 125

<210> 45
 <211> 424
 <212> PRT
 <213> Methanococcus jannaschii

<400> 45
 Met Gly Met Thr Ile Val Glu Lys Ile Leu Ala Lys Ala Ser Gly Lys
 1 5 10 15
 Lys Glu Val Ser Pro Gly Asp Ile Val Met Ala Asn Ile Asp Val Ala
 20 25 30
 Met Val His Asp Ile Thr Gly Pro Leu Thr Val Asn Thr Leu Lys Glu
 35 40 45
 Tyr Gly Ile Glu Lys Val Trp Asn Pro Glu Lys Ile Val Ile Leu Phe
 50 55 60
 Asp His Gln Val Pro Ala Asp Ser Ile Lys Ala Ala Glu Asn His Ile
 65 70 75 80
 Leu Met Arg Lys Phe Val Lys Glu Gln Gly Ile Lys Tyr Phe Tyr Asp
 85 90 95
 Ile Arg Glu Gly Val Cys His Gln Val Leu Pro Glu Lys Gly His Val
 100 105 110
 Ala Pro Gly Glu Val Val Val Gly Ala Asp Ser His Thr Cys Thr His
 115 120 125
 Gly Ala Phe Gly Ala Phe Ala Thr Gly Ile Gly Ser Thr Asp Met Ala
 130 135 140
 His Val Phe Ala Thr Gly Lys Leu Trp Phe Lys Val Pro Glu Thr Ile
 145 150 155 160

10027450-12001

10027450.12001

Tyr Phe Asn Ile Thr Gly Asp Leu Gln Pro Tyr Val Thr Ser Lys Asp
165 170 175

Val Ile Leu Ser Ile Ile Gly Glu Val Gly Val Asp Gly Ala Thr Tyr
180 185 190

Lys Ala Cys Gln Phe Gly Gly Glu Thr Val Lys Lys Met Ser Ile Ala
195 200 205

Ser Arg Met Thr Met Thr Asn Met Ala Ile Glu Met Gly Gly Lys Thr
210 215 220

Gly Ile Ile Glu Pro Asp Glu Lys Thr Ile Gln Tyr Val Lys Glu Ala
225 230 235 240

Met Lys Lys His Gly Thr Glu Arg Pro Phe Glu Val Ile Lys Gly Asp
245 250 255

Glu Asp Ala Glu Phe Ala Glu Val Tyr Glu Ile Glu Ala Asp Lys Ile
260 265 270

Glu Pro Val Phe Ala Cys Pro His Asn Val Asp Asn Val Lys Gln Ala
275 280 285

Arg Glu Val Ala Gly Lys Pro Ile Asp Gln Val Phe Ile Gly Ser Cys
290 295 300

Thr Asn Gly Arg Leu Glu Asp Leu Arg Met Ala Ile Lys Ile Ile Glu
305 310 315 320

Lys His Gly Gly Ile Ala Asp Asp Val Arg Val Val Val Thr Pro Ala
325 330 335

Ser Arg Glu Glu Tyr Leu Lys Ala Leu Lys Glu Gly Ile Ile Glu Lys
340 345 350

Phe Leu Lys Tyr Gly Cys Val Val Thr Asn Pro Ser Cys Ser Ala Cys
355 360 365

Met Gly Ser Leu Tyr Gly Val Leu Gly Pro Gly Glu Val Cys Val Ser
370 375 380

Thr Ser Asn Arg Asn Phe Arg Gly Arg Gln Gly Ser Leu Glu Ala Glu
385 390 395 400

Ile Tyr Leu Ala Ser Pro Ile Thr Ala Ala Ala Cys Ala Val Lys Gly
405 410 415

Glu Leu Val Asp Pro Arg Asp Leu
420

<210> 46
<211> 1033
<212> DNA
<213> Zea mays

<400> 46
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cgagctccaa ccagcgcgtt tatccggcgc tccagctca cctgtcatcg cctccactca 120
ctaaaatgcc gccgcgctgg gtccatcgtc cccgcggccg ctgctgcgcg ggcgggcagc 180
agctcgccgt cgtcagccgt tttccacggc gagtgttcg tgggtgggca caatatcgac 240
accgaccaga tcatccccgc cgagcacctc actctggtgc cctccaagcc ggacgagtac 300
cgcaagctcg gttccttcgc cttcgcgggg ctccatccg cggcctaccc gacgcggttc 360
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tgcggttcct ctgcgagca cgcgccgctc gcgcttgagg ccgctggcgc acgcgccatt 480
gttgcsagg gctacgcgcg catctttttt cgcaactccg tggccactgg agaggtgtac 540

cctctggagc tcacggacgt tggggcctgg aaggagtgca agacagggga tgtggtcacc 600
gtggaccttg ctaactccgt ttttattaac cacacctctg gcaaggagta caagctgaaa 660
ccaattggtg atgctggccc tgtaattgag gcgggagga tctttgccta cgcccgaag 720
acaggaatga ttgcgtcgaa agctgctgca tgagggaaa cttatgcagc cgagcctctg 780
cggagatgaa gaagtaagct ggagttagga ctaagagtta ctgcacctac ttgatgtcga 840
cgggtgtctca aaataagttg cggcctaccg aaattatgat gaatcaatca atttggctct 900
tgtcacagat cgtttttttt tgttactagt acttgtaaa ttgtactcct gcctgctact 960
gttcttatct gtttgaataa ctgctctgtt gccaaaaaaa aaaaaaaaaa aaaaaaaaaa 1020
aaaaaaaaaa aaa 1033

<210> 47
<211> 249
<212> PRT
<213> Zea mays

<400> 47
Met Ala Ala Ala Leu Ser Gly Thr Ala Val Ser Thr Ala Ala Leu Leu
1 5 10 15
Ala Pro Ile Arg Ala Pro Thr Ser Ala Phe Ile Arg Arg Ser Gln Leu
20 25 30
Thr Cys His Arg Leu His Ser Leu Lys Cys Arg Arg Ala Gly Ser Ile
35 40 45
Val Pro Ala Ala Ala Ala Ala Ala Gly Ser Ser Ser Pro Ser Ser
50 55 60
Ala Val Phe His Gly Glu Cys Phe Val Val Gly Asp Asn Ile Asp Thr
65 70 75 80
Asp Gln Ile Ile Pro Ala Glu His Leu Thr Leu Val Pro Ser Lys Pro
85 90 95
Asp Glu Tyr Arg Lys Leu Gly Ser Phe Ala Phe Ala Gly Leu Pro Ser
100 105 110
Ala Ala Tyr Pro Thr Pro Phe Val Ala Pro Gly Glu Glu Ser Ser Arg
115 120 125
Tyr Ala Ile Ile Val Gly Gly Ala Asn Phe Gly Cys Gly Ser Ser Arg
130 135 140
Glu His Ala Pro Val Ala Leu Gly Ala Ala Gly Ala Arg Ala Ile Val
145 150 155 160
Ala Glu Gly Tyr Ala Arg Ile Phe Phe Arg Asn Ser Val Ala Thr Gly
165 170 175
Glu Val Tyr Pro Leu Glu Leu Thr Asp Val Gly Ala Trp Lys Glu Cys
180 185 190
Lys Thr Gly Asp Val Val Thr Val Asp Leu Ala Asn Ser Val Phe Ile
195 200 205
Asn His Thr Ser Gly Lys Glu Tyr Lys Leu Lys Pro Ile Gly Asp Ala
210 215 220
Gly Pro Val Ile Glu Ala Gly Gly Ile Phe Ala Tyr Ala Arg Lys Thr
225 230 235 240
Gly Met Ile Ala Ser Lys Ala Ala Ala
245

<210> 48
<211> 1112

<212> DNA
<213> Oryza sativa

<400> 48
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tccttgcccg aggcggcgcc ggtgacagca gttctggcac cgtgtcccac gccctcgagg 120
acgttccgcc gccgcagctg ggtcgcggtt atctgccggc ccgccttgaa atgccaccac 180
agtcgtcccc tgaccgcccgt ggtcgccggt gctcgcggtg ccgctgcggc gggggactcg 240
acgtcgggccg gcgtattcca cggcgagtgc ttcgtcgtgg gggataacat cgacaccgac 300
cagatcatcc cggccgagca cctgaccctg gtcccgcca agcccagca gtaccgcaag 360
ctcggctcgt tcgccttcgt cggcctcccc accgcggcct acccgacgcc gttcgtcgcc 420
cccggcgagg agaccaccgc ctacgccgtc atcatcggtg gcgccaactt cggctgcggc 480
tcctcccgcg agcacgcgcc cgtcgccctg ggccgcggcg gcgcccgcgc cgtcgtggcc 540
gagggctacg cgcgcattct cttccgcaac tccgtggcca ccggtgaggt ctaccggtt 600
gagctagcgg acaactggagc ctggaaggag tgcaagaccg gggatgtggt cacggtggaa 660
cttgataatt gcgtcatgat caaccacaca tccggcaagc agtacaagct gaagcctatc 720
ggcgatgccg ggccggttat tgaggcaggc gggatctttg cctatgcccg gaagaccgga 780
atgatcgcat ccaagtctgc gtgagggaaa ggcgagtttg gtctgctgtc aagatagtcg 840
aggcctctgc agatagcaag taagactggg ttgtggattt gaacctattg cacctctatg 900
cgattgtcca tcagttgtac tgctgttttt acctaggttg tgtgtcatca gtggtgtttt 960
tggaataagt taaaagttac agagtactga actatgatgt attagtccat gtgatcttat 1020
gtaacacctt atgtaataca ctcgtttata cctgccgatt tgcctatctc gtttcgataa 1080
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa 1112

<210> 49
<211> 257
<212> PRT
<213> Oryza sativa

<400> 49
Met Ala Ala Ala Ala Ala Ala Pro Ala Leu Ser Leu Ala Glu Ala Ala
1 5 10 15
Pro Val Thr Ala Val Leu Ala Pro Cys Pro Thr Pro Ser Arg Thr Phe
20 25 30
Arg Arg Arg Ser Trp Val Ala Ala Ile Cys Arg Pro Ala Leu Lys Cys
35 40 45
His His Ser Arg Pro Leu Thr Ala Val Val Ala Ala Ala Ala Ala Ala
50 55 60
Ala Ala Ala Gly Asp Ser Thr Ser Ala Gly Val Phe His Gly Glu Cys
65 70 75 80
Phe Val Val Gly Asp Asn Ile Asp Thr Asp Gln Ile Ile Pro Ala Glu
85 90 95
His Leu Thr Leu Val Pro Ser Lys Pro Asp Glu Tyr Arg Lys Leu Gly
100 105 110
Ser Phe Ala Phe Val Gly Leu Pro Thr Ala Ala Tyr Pro Thr Pro Phe
115 120 125
Val Ala Pro Gly Glu Glu Thr Thr Arg Tyr Ala Val Ile Ile Gly Gly
130 135 140
Ala Asn Phe Gly Cys Gly Ser Ser Arg Glu His Ala Pro Val Ala Leu
145 150 155 160
Gly Ala Ala Gly Ala Arg Ala Val Val Ala Glu Gly Tyr Ala Arg Ile
165 170 175
Phe Phe Arg Asn Ser Val Ala Thr Gly Glu Val Tyr Pro Leu Glu Leu
180 185 190

Ala Asp Thr Gly Ala Trp Lys Glu Cys Lys Thr Gly Asp Val Val Thr
 195 200 205
 Val Glu Leu Asp Asn Cys Val Met Ile Asn His Thr Ser Gly Lys Gln
 210 215 220
 Tyr Lys Leu Lys Pro Ile Gly Asp Ala Gly Pro Val Ile Glu Ala Gly
 225 230 235 240
 Gly Ile Phe Ala Tyr Ala Arg Lys Thr Gly Met Ile Ala Ser Lys Ser
 245 250 255

Ala

<210> 50
 <211> 1107
 <212> DNA
 <213> Glycine max

<400> 50
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 cctctctca ctctcacact cttctaccgc gcttcccttc tttcccaact cccaagtcac 180
 caaacctctg caaccgcgtc gcagtctctc tccaaacccc acgcgctcaa tccgcgcgt 240
 ccgcttctcc ctccgcctcc ttccacggcc tctgctacgt cgtcggcgac aatatcgaca 300
 ccgaccagat cattcccgcc gagtacctca cctcgtccc ttccaagccc gacgagtacg 360
 agaagctcgg ctctacgcc ctcatcgcc tccccgccac ctacgccacg cgtttcatcg 420
 aaccggcgga gatcaaaacc aagtagccca tcgtcatcgg cgggtgccaac ttcggttgcg 480
 gctctcccg cgagcacgcc cccgtcgcgc tgggcgcctc cggcgccgcc gcagtggcg 540
 cggagtcgta cgctaggatc ttctttcgga actccgtggc caccggcgag gtgtatccgc 600
 tagagtcgga gggacgcctc tgcgaggagt gcaccaccgg cgatgtggtg acgattgagc 660
 tcggagagag ccgcttgatc aatcacacca ccgaaaagga gtatcgcttg aaaccgatcg 720
 gcgacgcggg tccagtgatc gaggccggtg gcatctttgc ctatgccagg aaaaccggca 780
 tgattccctc tcgttgagtt cttcaggtga gggcagtga ctctgctatc cttgcttcag 840
 atgacatgct tctcaagaaa tgtattgacc caatggatgc cttagcttgg tccattatca 900
 aataggctag aacttgacga gatataatac atggcaatag aaagtgtgtt ttaatggttc 960
 ttgcatcagc agcttctttt ataatctcat tgatatgggg tatctcatta atgcaaactt 1020
 ttgtattcac gaaatgggac caattttgcc ccatttatca atcagaatgg tacttatttt 1080
 tcctcgggca aaaaaaaaaa aaaaaaag 1107

<210> 51
 <211> 263
 <212> PRT
 <213> Glycine max

<220>
 <221> UNSURE
 <222> (4)

<400> 51
 Met Arg Lys Xaa Thr Glu Val Arg Glu Glu Ala Leu Ser Ile Gln Gln
 1 5 10 15
 Trp Pro Cys Thr Arg Phe Ser Ser Ala Ala Thr Val Leu Pro Arg Asn
 20 25 30
 Leu Ala Phe Thr Lys Leu Ser Leu Ser His Ser His Thr Leu Leu Pro
 35 40 45
 Arg Phe Leu Ser Phe Pro Thr Pro Lys Ser Ser Asn Pro Arg Asn Arg
 50 55 60
 Val Ala Val Ser Leu Gln Thr Pro Arg Ala Gln Ser Ala Ala Ser Ala
 65 70 75 80

Ser Pro Ser Ala Ser Phe His Gly Leu Cys Tyr Val Val Gly Asp Asn
 85 90 95
 Ile Asp Thr Asp Gln Ile Ile Pro Ala Glu Tyr Leu Thr Leu Val Pro
 100 105 110
 Ser Lys Pro Asp Glu Tyr Glu Lys Leu Gly Ser Tyr Ala Leu Ile Gly
 115 120 125
 Leu Pro Ala Thr Tyr Ala Thr Arg Phe Ile Glu Pro Gly Glu Ile Lys
 130 135 140
 Thr Lys Tyr Ala Ile Val Ile Gly Gly Ala Asn Phe Gly Cys Gly Ser
 145 150 155 160
 Ser Arg Glu His Ala Pro Val Ala Leu Gly Ala Ser Gly Ala Ala Ala
 165 170 175
 Val Val Ala Glu Ser Tyr Ala Arg Ile Phe Phe Arg Asn Ser Val Ala
 180 185 190
 Thr Gly Glu Val Tyr Pro Leu Glu Ser Glu Gly Arg Leu Cys Glu Glu
 195 200 205
 Cys Thr Thr Gly Asp Val Val Thr Ile Glu Leu Gly Glu Ser Arg Leu
 210 215 220
 Ile Asn His Thr Thr Gly Lys Glu Tyr Arg Leu Lys Pro Ile Gly Asp
 225 230 235 240
 Ala Gly Pro Val Ile Glu Ala Gly Gly Ile Phe Ala Tyr Ala Arg Lys
 245 250 255
 Thr Gly Met Ile Pro Ser Arg
 260

<210> 52
 <211> 995
 <212> DNA
 <213> Triticum aestivum

<400> 52
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 ggggtccatcg tccccgcggc cgctgctgcc gcggcgggca gcagctcgcc gtcgtcagcc 180
 gttttccacg gcgagtgtt cgtggtgggc gacaatatcg acaccgacca gatcatcccc 240
 gccgagcacc tcaactctgtt gccctccaag ccggacgagt accgcaagct cggttccttc 300
 gccttcgcgg ggctcccatc cgcggcctac ccgacgccgt tcgtcgctcc gggtgaggag 360
 tcctcccgt acgccatcat tgtcggcgga gccaaacttc ggtgcgggtc ctctcgcgag 420
 cacgcgcccg tcgcgcttgg ggccgctggc gcacgcgcca ttggtgcgga gggctacgcg 480
 cgcattttt ttgcgaactc cgtgggcaact ggagaggtgt accctctgga gctcacggac 540
 gttggggcct ggaaggagt caagacagg gatgtgttca ccgtggacct tgctaactcc 600
 gtttttatta accacacctc tggcaaggag tacaagctga aaccaattgg tgatgctggc 660
 cctgtaattg aggcgggagg gatctttgcc tacgcccga agacaggaat gattgcgtcg 720
 aaagctgctg catgaggga agatcagctt atgcagccga gcctctgcgg agatgaagaa 780
 gtaagctgga gttaggacta agagttactg cacctacttg atgtcgacgg tgtctcaaaa 840
 taagttgcgg cctaccgaaa ttatgatgaa tcaatcaatt tggctcttgt cacagatcgt 900
 ttttttttgt tactagtact tgtacaattg tactcctgcc tgctactgtt cttatctgtt 960
 tgaataactg ctctgttgcc atctaaaaaa aaaaaa 995

<210> 53
 <211> 244
 <212> PRT
 <213> Triticum aestivum

<400> 53
 Ala Arg Ala Ala Val Ser Thr Ala Ala Leu Leu Ala Pro Ile Arg Ala
 1 5 10 15
 Pro Thr Ser Ala Phe Ile Arg Arg Ser Gln Leu Thr Cys His Arg Leu
 20 25 30
 His Ser Leu Lys Cys Arg Arg Ala Gly Ser Ile Val Pro Ala Ala Ala
 35 40 45
 Ala Ala Ala Ala Gly Ser Ser Ser Pro Ser Ser Ala Val Phe His Gly
 50 55 60
 Glu Cys Phe Val Val Gly Asp Asn Ile Asp Thr Asp Gln Ile Ile Pro
 65 70 75 80
 Ala Glu His Leu Thr Leu Val Pro Ser Lys Pro Asp Glu Tyr Arg Lys
 85 90 95
 Leu Gly Ser Phe Ala Phe Ala Gly Leu Pro Ser Ala Ala Tyr Pro Thr
 100 105 110
 Pro Phe Val Ala Pro Gly Glu Glu Ser Ser Arg Tyr Ala Ile Ile Val
 115 120 125
 Gly Gly Ala Asn Phe Gly Cys Gly Ser Ser Arg Glu His Ala Pro Val
 130 135 140
 Ala Leu Gly Ala Ala Gly Ala Arg Ala Ile Val Ala Glu Gly Tyr Ala
 145 150 155 160
 Arg Ile Phe Phe Arg Asn Ser Val Gly Thr Gly Glu Val Tyr Pro Leu
 165 170 175
 Glu Leu Thr Asp Val Gly Ala Trp Lys Glu Cys Lys Thr Gly Asp Val
 180 185 190
 Val Thr Val Asp Leu Ala Asn Ser Val Phe Ile Asn His Thr Ser Gly
 195 200 205
 Lys Glu Tyr Lys Leu Lys Pro Ile Gly Asp Ala Gly Pro Val Ile Glu
 210 215 220
 Ala Gly Gly Ile Phe Ala Tyr Ala Arg Lys Thr Gly Met Ile Ala Ser
 225 230 235 240
 Lys Ala Ala Ala

<210> 54
 <211> 113
 <212> PRT
 <213> Lactococcus lactis

<400> 54
 Met Lys Thr Tyr Lys Gly Thr Ser Val Val Met Asn Asp Asn Asp Thr
 1 5 10 15
 Asp Lys Lys Ala Asp Lys Lys Gly Gly Lys Asn Tyr Trp Arg Tyr Lys
 20 25 30
 Asp Tyr Asp Asn Asp Asn Ala Lys Tyr Lys Lys Ala Ser Ser Gly Asp
 35 40 45
 Asn Gly Ser Gly Ser Ser Arg His Ala Ala Trp Ala Ser Asp Tyr Gly
 50 55 60

Arg Ala Ala Gly Ser Tyr Ser Asp Tyr Asn Asn Ala Lys Asn Gly Lys
65 70 75 80

Arg Val Asn Thr Lys Ser Ser Thr Asp His Thr Ser Gly Asp His Asp
85 90 95

Trp Lys Asp Lys Asn Gly Asp Asp Gly Thr Tyr Ala Ser Ala Tyr Lys
100 105 110

Asn

10027450-12001